

Amendments to the Claims

This listing of claims will replace all prior versions, and listings, of claims in the application:

1. (Currently Amended) A ~~[[M]]~~method for in vitro detection of acute generalized inflammatory conditions (SIRS), comprising:

~~characterized in that~~

~~it comprises the following steps:~~

~~Isolation of~~ isolating sample RNA from a sample of a mammal;

~~[[L]]~~labelling of the sample RNA and/or at least one DNA being a gene or gene fragment specific for SIRS, with a detectable label.

~~[[C]]~~contacting the sample RNA with the DNA under hybridization conditions;

~~[[C]]~~contacting sample RNA representing a control for non-pathologic conditions, with at least one DNA, under hybridization conditions, whereby the DNA is a gene or gene fragment specific for SIRS;

~~[[Q]]~~quantitative detection of the label signals of the hybridized sample RNA and control RNA; and

~~[[C]]~~comparing the quantitative data of the label signals in order to determine whether the genes or gene fragments specific for SIRS are more expressed in the sample than in the control, or less.

2. (Currently Amended) A ~~[[M]]~~method for in vitro detection of sepsis and/or sepsis-like conditions,

~~characterized in that~~

~~it comprises the following steps:~~

~~Isolation~~ isolating of sample RNA from a sample of a mammal;

~~[[L]]labelling of the sample RNA and/or at least one DNA being a gene or gene fragment specific for sepsis, with a detectable label.~~

~~[[C]]contacting the sample RNA with the DNA under hybridization conditions;~~

~~[[C]]contacting sample RNA representing a control for non-pathologic conditions, with at least one DNA, under hybridization conditions, whereby the DNA is a gene or gene fragment specific for sepsis and/or sepsis-like conditions;~~

~~[[Q]]quantitative detection of the label signals of the hybridized sample RNA and control RNA; and~~

~~[[C]]comparing the quantitative data of the label signals in order to determine whether the genes or gene fragments specific for sepsis and/or sepsis-like conditions are more expressed in the sample than in the control, or less.~~

3. (Currently Amended) A ~~[[M]]method~~ for in vitro detection of severe sepsis, comprising:

~~characterized in that~~

~~it comprises the following steps:~~

~~Isolation~~ isolating of sample RNA from a sample of a mammal;

~~[[L]]labelling of the sample RNA and/or at least one DNA being a gene or gene fragment specific for severe sepsis, with a detectable label.~~

~~[[C]]contacting the sample RNA with the DNA under hybridization conditions;~~

[[C]]ontacting sample RNA representing a control for non-pathologic conditions, with at least one DNA, under hybridization conditions, whereby the DNA is a gene or gene fragment specific for severe sepsis;

[[Q]]uantitative detection of the label signals of the hybridized sample RNA and control RNA; and

[[C]]omparing the quantitative data of the label signals in order to determine whether the genes or gene fragments specific for severe sepsis are more expressed in the sample than in the control, or less.

4. (Currently Amended) The [[M]]ethod ~~according to one~~ of claim[[s]] 1 [[to 3]], characterized in that the control RNA is hybridized with the DNA before the measurement of the sample RNA and the label signals of the control RNA/DNA-complex is gathered and, if necessary, recorded in form of a calibration curve or table.
5. (Currently Amended) The [[M]]ethod ~~according to one~~ of claim[[s]] 1 [[to 4]], characterized in that unchanged genes from sample and/or control RNA are used as reference genes for the quantification.
6. (Currently Amended) The [[M]]ethod ~~according to one~~ of claim[[s]] 1 [[to 5]], characterized in that mRNA is used as sample RNA.
7. (Currently Amended) The [[M]]ethod ~~according to one~~ of claim[[s]] 1 [[to 6]], characterized in that the DNA is arranged, particularly immobilized, on predetermined areas on a carrier in the form of a microarray.
8. (Currently Amended) The [[M]]ethod ~~according to one~~ of claim[[s]] 1 [[to 7]], characterized in that the method for early detection by means of differential diagnostics, for control of the clinical and therapeutic progress, for the individual risk evaluation in patients, for the evaluation whether the patient will respond to a specific treatment, as well as for post mortem diagnosis of SIRS and/or sepsis and/or severe sepsis and/or systemic infections and/or septic conditions and/or infections.

9. (Currently Amended) The ~~[[M]]method according to one~~ of claim[[s]] 1 ~~[[to 8]],~~ characterized in that the sample is selected from the following group: body fluids, in particular blood, liquor, urine, ascitic fluid, seminal fluid, saliva, puncture fluid, cell content, or a mixture thereof.
10. (Currently Amended) The ~~[[M]]method according to one~~ of claim[[s]] 1 ~~[[to 9]],~~ characterized in that cell samples are subjected a lytic treatment, if necessary, in order to free their cell contents.
11. (Currently Amended) The ~~[[M]]method according to one~~ of claim[[s]] 1 ~~[[to 10]],~~ characterized in that the mammal is a human.
12. (Currently Amended) The ~~[[M]]method according to one~~ of claim[[s]] 1 ~~or 4 to 11,~~ characterized in that the gene or gene segment specific for SIRS is selected from the group consisting of SEQUENCE ID No. III.1 to SEQUECE ID No. III.4168, as well as gene fragments thereof with 5-2000 or more, preferably 20-200, more preferably 20-80 nucleotides.
13. (Currently Amended) The ~~[[M]]method according to one~~ of claim[[s]] 2 ~~or 4 to 11,~~ characterized in that the gene or gene segment specific for sepsis and/or sepsis-like conditions is selected from the group consisting of SEQUENCE ID No. I.1 to SEQUECE ID No. I.6242, as well as gene fragments thereof with 5-2000 or more, preferably 20-200, more preferably 20-80 nucleotides.
14. (Currently Amended) The ~~[[M]]method according to one~~ of claim[[s]] 3 ~~or 4 to 11,~~ characterized in that the gene or gene segment specific for severe sepsis is selected from the group consisting of SEQUENCE ID No. II.1 to SEQUECE ID No. II.130, as well as gene fragments thereof with 5-2000 or more, preferably 20-200, more preferably 20-80 nucleotides.
15. (Currently Amended) The ~~[[M]]method according to one~~ of claim[[s]] 1 ~~[[to 14]],~~ characterized in that at least 2 to 100 different cDNAs are used.
16. (Currently Amended) The ~~[[M]]method according to one~~ of claim[[s]] 1 ~~[[to 15]],~~ characterized in that at least 200 different cDNAs are used.

17. (Currently Amended) The ~~[[M]]method according to one~~ of claim[[s]] 1 ~~[[to 16]]~~, characterized in that at least 200 to 500 different cDNAs are used.
18. (Currently Amended) The ~~[[M]]method according to one~~ of claim[[s]] 1 ~~[[to 17]]~~, characterized in that at least 500 to 1000 different cDNAs are used.
19. (Currently Amended) The ~~[[M]]method according to one~~ of claim[[s]] 1 ~~[[to 18]]~~, characterized in that at least 1000 to 2000 different cDNAs are used.
20. (Currently Amended) The ~~[[M]]method according to one~~ of claim[[s]] 1 ~~[[to 19]]~~, characterized in that the cDNA of ~~the genes listed in claims 12, 13 and 14~~ is SEQUENCE ID No. III.1 to SEQUECE ID No. III.4168, SEQUENCE ID No. I.1 to SEQUECE ID No. I.6242 and SEQUENCE ID No. II.1 to SEQUECE ID No. II.130 replaced by synthetic analogs as well as peptidonucleic acids.
21. (Currently Amended) The ~~[[M]]method according to~~ of claim 20, characterized in that the synthetic analogs of the listed genes comprise 5-100, in particular approximately 70, base pairs.
22. (Currently Amended) The ~~[[M]]method according to one~~ of claim[[s]] 1 ~~[[to 21]]~~, characterized in that a radioactive label, in particular ^{32}P , ^{14}C , ^{125}I , ~~[[^{155}Eu]]~~ ^{155}Eu , ^{33}P or ^3H is used as detectable label.
23. (Currently Amended) The ~~[[M]]method according to one~~ of claim[[s]] 1 ~~[[to 22]]~~, characterized in that a non-radioactive label is used as detectable label, in particular a color- or fluorescence label, an enzyme label or immune label, and/or quantum dots or an electrically measurable signal, in particular the change in potential, and/or conductivity and/or capacity by hybridizations.
24. (Currently Amended) The ~~[[M]]method according to one~~ of claim[[s]] 1 ~~[[to 23]]~~, characterized in that the sample RNA and control RNA bear the same label.
25. (Currently Amended) The ~~[[M]]method according to one~~ of claim[[s]] 1 ~~[[to 24]]~~, characterized in that the sample RNA and control RNA bear different labels.

26. (Currently Amended) The ~~[[M]]method according to one~~ of claim[[s]] 1 ~~[[to 25]]~~, characterized in that the immobilized probes bear a label.
27. (Currently Amended) The ~~[[M]]method according to one~~ of claim[[s]] 1 ~~[[to 26]]~~, characterized in that the cDNA probes are immobilized on glass or plastics.
28. (Currently Amended) The ~~[[M]]method according to one~~ of claim[[s]] 1 ~~[[to 27]]~~, characterized in that the individual cDNA molecules are immobilized on the carrier material by means of a covalent binding.
29. (Currently Amended) The ~~[[M]]method according to one~~ of claim[[s]] 1 ~~[[to 28]]~~, characterized in that the individual cDNA molecules are immobilized onto the carrier material by means of adsorption, in particular by means of electrostatic and/or dipole-dipole and/or hydrophobic interactions and/or hydrogen bridges.
30. (Currently Amended) A ~~[[M]]method for in vitro detection of SIRS, comprising:~~
~~characterized in that~~
~~it comprises the following steps:~~
~~Isolation of isolating~~ sample peptides from a sample of a mammal;
~~[[L]]labelling of the sample peptides with a detectable label;~~
~~[[C]]contacting the labelled sample peptides with at least one antibody or its binding fragment, whereby the antibody binds a peptide or peptide fragment specific for SIRS;~~
~~[[C]]contacting the labelled control peptides originating from healthy subjects, with at least one antibody or its binding fragment immobilized on a carrier in form of a microarray, whereby the antibody binds a peptide or peptide fragment specific for SIRS;~~
~~[[Q]]quantitative detection of the label signals of the sample peptides and the control peptides;~~

[[C]]comparing the quantitative data of the label signals in order determine whether the genes or gene fragments specific for SIRS are more expressed in the sample than in the control, or less.

31. (Currently Amended) A [[M]]method for in vitro detection of sepsis and/or sepsis-like conditions, comprising:

~~characterized in that~~

~~it comprises the following steps:~~

~~Isolation of isolating~~ sample peptides from a sample of a mammal;

[[L]]labelling of the sample peptides with a detectable label;

[[C]]contacting the labelled sample peptides with at least one antibody or its binding fragment, whereby the antibody binds a peptide or peptide fragment specific for sepsis and/or sepsis-like conditions;

[[C]]contacting the labelled control peptides stemming from healthy subjects, with at least one antibody or its binding fragment immobilized on a carrier in form of a microarray, whereby the antibody binds a peptide or peptide fragment specific for sepsis and/or sepsis-like conditions;

[[Q]]quantitative detection of the label signals of the sample peptides and the control peptides; and

[[C]]comparing the quantitative data of the label signals in order to be able to determine whether the genes or gene fragments specific for sepsis and/or sepsis-like conditions are more expressed in the sample than in the control, or less.

32. (Currently Amended) A [[M]]method for in vitro detection of severe sepsis, comprising:

~~characterized in that~~

~~it comprises the following steps:~~

~~Isolation of isolating~~ sample peptides from a sample of a mammal;

[[L]]labelling of the sample peptides with a detectable label;

[[C]]contacting the labelled sample peptides with at least one antibody or its binding fragment, whereby the antibody binds a peptide or peptide fragment specific for severe sepsis;

[[C]]contacting the labelled control peptides originating from healthy subjects, with at least one antibody or its binding fragment immobilized on a carrier in form of a microarray, whereby the antibody binds a peptide or peptide fragment specific for severe sepsis;

[[Q]]quantitative detection of the label signals of the sample peptides and the control peptides; and

[[C]]comparing the quantitative data of the label signals in order to determine whether the genes or gene fragments specific for severe sepsis are more expressed in the sample than in the control, or less.

33. (Currently Amended) The [[M]]method ~~according to one~~ of claim[[s]] 30 [[to 32]], characterized in that the antibody is immobilized on an array in form of a microarray.
34. (Currently Amended) The [[M]]method ~~according to one~~ of claim[[s]] 30 [[to 33]], characterized in that it is formed as immunoassay.
35. (Currently Amended) The [[M]]method ~~according to one~~ of claim[[s]] 30 [[to 34]], characterized in that the method is used for early detection by means of differential diagnostics, for control of the clinic and therapeutic progress, for risk evaluation for patients as well as for post mortem diagnosis of SIRS and/or sepsis and/or severe sepsis and/or systemic infections and/or septic conditions and/or infections.
36. (Currently Amended) The [[M]]method ~~according to one~~ of claim[[s]] 30 [[to 35]], characterized in that the sample is selected from the following group: body fluids, in particular blood, liquor, urine, ascitic fluid, seminal fluid, saliva, puncture fluid, cell content, or a mixture thereof.

37. (Currently Amended) The ~~[[M]]method according to one~~ of claim[[s]] 30 ~~[[to 36]],~~ characterized in that cell samples are subjected a lytic treatment, if necessary, in order to free their cell contents.
38. (Currently Amended) The ~~[[M]]method according to one~~ of claim[[s]] 30 ~~[[to 37]],~~ characterized in that the mammal is a human.
39. (Currently Amended) The ~~[[M]]method according to one~~ of claim[[s]] 30 ~~or 33 to 38,~~ characterized in that the peptide specific for SIRS is an expression product of a gene or gene fragment selected from the group consisting of SEQUENCE ID No. III.1 to SEQUECE ID No. III.4168, as well as gene fragments thereof with 5-2000 nucleotides or more, preferably 20-200, more preferable 20-80 nucleotides.
40. (Currently Amended) The ~~[[M]]method according to one~~ of claim[[s]] 31 ~~or 33 to 38,~~ characterized in that the peptide specific for sepsis and/or sepsis-like conditions is an expression product of a gene or gene fragment selected from the group consisting of SEQUENCE ID No. I.1 to SEQUECE ID No. I.6242, as well as gene fragments thereof with 5-2000 nucleotides or more, preferably 20-200, more preferable 20-80 nucleotides.
41. (Currently Amended) The ~~[[M]]method according to one~~ of claim[[s]] 32 ~~or 33 to 38,~~ characterized in that the peptide specific for severe sepsis is an expression product of a gene or gene fragment selected from the group consisting of SEQUENCE ID No. II.1 to SEQUECE ID No. II.130, as well as gene fragments thereof with 5-2000 or more, preferably 20-200, more preferably 20-80 nucleotides.
42. (Currently Amended) The ~~[[M]]method according to one~~ of claim[[s]] 30 ~~[[to 41]],~~ characterized in that at least 2 to 100 different peptides are used.
43. (Currently Amended) The ~~[[M]]method according to one~~ of claim[[s]] 30 ~~[[to 42]],~~ characterized in that at least 200 different peptides are used.
44. (Currently Amended) The ~~[[M]]method according to one~~ of claim[[s]] 30 ~~[[to 43]],~~ characterized in that at least 200 to 500 different peptides are used.

45. (Currently Amended) The [[M]]method ~~according to one~~ of claim[[s]] 30 ~~[[to 44]]~~, characterized in that at least 500 to 1000 different peptides are used.
46. (Currently Amended) The [[M]]method ~~according to one~~ of claim[[s]] 30 ~~to 45~~, characterized in that at least 1000 to 2000 different peptides are used.
47. (Currently Amended) The [[M]]method ~~according to one~~ of claim[[s]] 30 ~~[[to 46]]~~, characterized in that a radioactive label, in particular ^{32}P , ^{14}C , ^{125}I , [[^{155}Eu]] ~~^{155}Eu~~ , ^{33}P or ^3H is used as detectable label.
48. (Currently Amended) The [[M]]method ~~according to one~~ of claim[[s]] 30 ~~[[to 47]]~~, characterized in that a non-radioactive label is used as detectable label, in particular a color- or fluorescence label, an enzyme label or immune label, and/or quantum dots or an electrically measurable signal, in particular the change in potential, and/or conductivity and/or capacity by hybridizations.
49. (Currently Amended) The [[M]]method ~~according to one~~ of claim[[s]] 30 ~~[[to 48]]~~, characterized in that the sample peptides and control peptides bear the same label.
50. (Currently Amended) The [[M]]method ~~according to one~~ of claim[[s]] 30 ~~[[to 49]]~~, characterized in that the sample peptides and control peptides bear different labels.
51. (Currently Amended) The [[M]]method ~~according to one~~ of claim[[s]] 30 ~~[[to 50]]~~, characterized in that the probes used are peptides to which labelled antibodies are bound, which cause a change of signal of the labelled antibodies by change of conformation when binding to the sample peptides.
52. (Currently Amended) The [[M]]method ~~according to one~~ of claim[[s]] 30 ~~[[to 51]]~~, characterized in that the peptide probes are immobilized on glass or plastics.
53. (Currently Amended) The [[M]]method ~~according to one~~ of claim[[s]] 30 ~~[[to 52]]~~, characterized in that the individual peptide molecules are immobilized onto the carrier material by means of a covalent binding.

54. (Currently Amended) The ~~[[M]]method according to one~~ of claim[[s]] 30 ~~[[to 53]],~~ characterized in that the individual peptide molecules are immobilized on the carrier material by means of adsorption, in particular by means of electrostatic and/or dipole-dipole and/or hydrophobic interactions and/or hydrogen bridges.
55. (Currently Amended) The ~~[[M]]method according to one~~ of claim[[s]] 30 ~~[[to 54]],~~ characterized in that the individual peptide molecules are detected by means of monoclonal antibodies or their binding fragments.
56. (Currently Amended) The ~~[[M]]method according to one~~ of claim[[s]] 30 ~~[[to 55]],~~ characterized in that the determination of individual peptides by means of immunoassay or precipitation assay is carried out using monoclonal antibodies.
57. (Cancelled)
58. (Cancelled)
59. (Cancelled)